

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/167,705A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of <213>Organism Sequence(s) _____ are missing this mandatory field or its response.
(NEW RULES)
- 12 ☒ Use of <220>Feature Sequence(s) 1-6 are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/167,705DATE: 09/02/1999
TIME: 13:12:04

Input Set: I167705.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

Designation of Comply
Corrected Diskette Needed

1 <110> APPLICANT: Schmidt, Ann Marie
2 Stern, David
3 <120> TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND
4 USES THEREOF
5 <130> FILE REFERENCE: 0575-55873
6 <140> CURRENT APPLICATION NUMBER: US/09/167,705
7 <141> CURRENT FILING DATE: 1998-10-06
8 <160> NUMBER OF SEQ ID NOS: 6
9 <170> SOFTWARE: PatentIn Ver. 2.0
10 <210> SEQ ID NO 1
11 <211> LENGTH: 395
12 <212> TYPE: DNA
13 <213> ORGANISM: SEQ1
14 <400> SEQUENCE: 1
15 atgactaagc tggaggacca cctggaggga atcatcaaca tcttccacca gtactccgtt 60
16 cgggtggggc atttcgacac cctcaacaag cgtgagctga agcagctgat cacaaagggg 120
17 acttcccaaa accctccaga acaccaaaga ccaacctacc attgacaaaa tattccaaga 180
18 cctggatgcc gataaagacg gagccgtcag ctttgaggaa ttcgtagtcc tgggtgtccag 240
19 ggtgctgaaa acagcccaca tagatatcca caaagagtag gtttccagca atgttcccaa 300
20 gaagacttac ctttctcctc cctgaggctg ctccccgagg gagagagaat tataaacgta 360
21 ctttggcaaa ttcttagcaa aaaaaaaaaa aaaaa 395
22 <210> SEQ ID NO 2
23 <211> LENGTH: 50
24 <212> TYPE: PRT
25 <213> ORGANISM: SEQ2
26 <400> SEQUENCE: 2
27 Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Gly His Gln
28 1 5 10 15
29 Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Tyr Glu Leu
30 20 25 30
31 Lys Gln Leu Gly Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Xaa Lys
32 35 40 45
33 Asp Gln
34 50
35 <210> SEQ ID NO 3
36 <211> LENGTH: 90
37 <212> TYPE: PRT
38 <213> ORGANISM: SEQ3
39 <400> SEQUENCE: 3
40 Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His Gln
41 1 5 10 15
42 Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu
43 20 25 30
44 Lys Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys

The only valid responses, per sequence Rules, are: Artificial Sequence, Unknown, or Scientific name (Genus/Species), see circled portion of item 12 or Enron summary sheet

see item 10 or Enron summary sheet

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RAW SEQUENCE LISTING
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45           35           40           45
46      Asp Gln Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp Lys
47           50           55           60
48      Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val
49           65           70           75           80
50      Leu Lys Thr Ala His Ile Asp Ile His Lys
51           85           90
52 <210> SEQ ID NO 4
53 <211> LENGTH: 90
54 <212> TYPE: PRT
55 <213> ORGANISM: SEQ4
56 <400> SEQUENCE: 4
57      Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His Gln
58           1           5           10           15
59      Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu
60           20           25           30
61      Lys Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys
62           35           40           45
63      Asp Gln Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp Lys
64           50           55           60
65      Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val
66           65           70           75           80
67      Leu Lys Thr Ala His Ile Asp Ile His Lys
68           85           90
69 <210> SEQ ID NO 5
70 <211> LENGTH: 18
71 <212> TYPE: PRT
72 <213> ORGANISM: SEQ5
73 <400> SEQUENCE: 5
74      Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val
75           1           5           10           15
76      Leu Lys
77 <210> SEQ ID NO 6
78 <211> LENGTH: 5
79 <212> TYPE: PRT
80 <213> ORGANISM: SEQ6
81 <400> SEQUENCE: 6
82      Ala Gln Asn Ile Thr
83           1           5

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VERIFICATION SUMMARY
PATENT APPLICATION US/09/167,705

DATE: 09/02/1999
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Line ? Error/Warning

Original Text

31 W "N" or "Xaa" used: Feature required

Lys Gln Leu Gly Thr Lys Glu Leu Pro Lys T